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SEQUENCE LISTING

<110> Università degli Studi di Roma "La Sapienza"
Consiglio Nazionale delle Ricerche

<120> Purification, cloning and biochemical characterization of XendoU,
endoribonucleasic activity involved in Xenopus laevis small
nuclear RNA splicing independent biosynthesis

<130> PCT25390

<150> IT RM2002A000365
<151> 2002-07-08

<160> 9

<170> PatentIn version 3.2

<210> 1
<211> 1265
<212> DNA
<213> Xenopus laevis

<220>
<221> misc_feature
<222> (1)..(38)
<223> 5' untranslated DNA region

<220>
<221> exon
<222> (39)..(915)

<220>
<221> terminator
<222> (916)..(918)

<220>
<221> misc_feature
<222> (916)..(1265)
<223> 3' untranslated DNA region

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atggggAAC tgggAGCAGA gagtgacGGG caggAGCC atg gCG agt aAC agg gGG 56
Met Ala Ser Asn Arg Gly
1 5

cag ctg aac cat gaa ctc tcc aag ctg ttt aat gag ctg tgg gac gca 104
Gln Leu Asn His Glu Leu Ser Lys Leu Phe Asn Glu Leu Trp Asp Ala
10 15 20

gat cag aac cgg atg aag tcc ggg aag gat tat cgg atc tcc ttg cag 152
Asp Gln Asn Arg Met Lys Ser Gly Lys Asp Tyr Arg Ile Ser Leu Gln
25 30 35

ggT aaa gca ggg tac gta ccc gcc ggt tcc aac cag gcc agg gac agc 200
Gly Lys Ala Gly Tyr Val Pro Ala Gly Ser Asn Gln Ala Arg Asp Ser

40

45

50

gcc tcg ttc ccg ctc ttc cag ttc gtc gat gag gag aag ctg aag agc	248
Ala Ser Phe Pro Leu Phe Gln Phe Val Asp Glu Glu Lys Leu Lys Ser	
55 60 65 70	
agg aag acg ttt gca acc ttc att tcc ctg ctg gac aat tat gag atg	296
Arg Lys Thr Phe Ala Thr Phe Ile Ser Leu Leu Asp Asn Tyr Glu Met	
75 80 85	
gac acg ggg gtg gcc gag gtt gtg act ccg gag gaa atc gct gaa aac	344
Asp Thr Gly Val Ala Glu Val Val Thr Pro Glu Glu Ile Ala Glu Asn	
90 95 100	
aac aac ttc ctg gac gcc att ctg gaa acc aaa gtg atg aag atg gca	392
Asn Asn Phe Leu Asp Ala Ile Leu Glu Thr Lys Val Met Lys Met Ala	
105 110 115	
cat gac tac ctg gtg agg aag aac caa gcc aaa ccc acc cgg aat gac	440
His Asp Tyr Leu Val Arg Lys Asn Gln Ala Lys Pro Thr Arg Asn Asp	
120 125 130	
ttc aag gtc caa ctg tac aac atc tgg ttc cag ctg tac tca cgg gcc	488
Phe Lys Val Gln Leu Tyr Asn Ile Trp Phe Gln Leu Tyr Ser Arg Ala	
135 140 145 150	
cca ggg agc aga ccc gat tcg tgc ggc ttt gag cac gtg ttt gtg gga	536
Pro Gly Ser Arg Pro Asp Ser Cys Gly Phe Glu His Val Phe Val Gly	
155 160 165	
gaa tcg aag cga ggg cag gag atg atg ggg ctt cac aac tgg gtc cag	584
Glu Ser Lys Arg Gly Gln Glu Met Met Gly Leu His Asn Trp Val Gln	
170 175 180	
ttt tac ctt cag gag aag agg aag aac atc gac tat aaa gga tac gtg	632
Phe Tyr Leu Gln Glu Lys Arg Lys Asn Ile Asp Tyr Lys Gly Tyr Val	
185 190 195	
gct cgg cag aac aag agt cgg ccg gat gaa gat gat cag gtg ttg aac	680
Ala Arg Gln Asn Lys Ser Arg Pro Asp Glu Asp Asp Gln Val Leu Asn	
200 205 210	
ctg cag ttc aat tgg aag gag atg gtg aaa ccc gtc ggc agc agc ttc	728
Leu Gln Phe Asn Trp Lys Glu Met Val Lys Pro Val Gly Ser Ser Phe	
215 220 225 230	
att ggc gtc agc ccg gaa ttc gaa ttc gcc ctt tac acc atc gtc ttc	776
Ile Gly Val Ser Pro Glu Phe Glu Phe Ala Leu Tyr Thr Ile Val Phe	
235 240 245	
ctc gcg tct cag gag aag atg agc cga gaa gtc gtt cgg ctg gaa gaa	824
Leu Ala Ser Gln Glu Lys Met Ser Arg Glu Val Val Arg Leu Glu Glu	
250 255 260	
tac gaa ctg cag atc gtc gtc aat cgc cac ggc cgt tat ata ggg acc	872
Tyr Glu Leu Gln Ile Val Val Asn Arg His Gly Arg Tyr Ile Gly Thr	
265 270 275	

gcc tac ccc gtc ctc ctg agc acc aat aac ccg gat ctg tac t 915
Ala Tyr Pro Val Leu Leu Ser Thr Asn Asn Pro Asp Leu Tyr
280 285 290

gagggggcgg ggctagagat cacagccgtt tcccacggtt tgggtgcatt tactaacaaa 975

actgcaccaa tgcaacaatg caagcagata atggggcag gtccatatcc ctctgcttc 1035

cctagcgtgt gtggggcaca ttaaccctat aactgtcact cactgcacca gaccattat 1095

ttaacccac aagggacatc aagccagtgc cttgttatga gagagcgcag ccggggcttc 1155

tctactgtga aacttctgta ttgtatagag tttacttggt ttcttcctcc agacaatttc 1215

acttttttt tgctttgcct ttaaccatta aaagtccatg acatttctgt 1265

<210> 2

<211> 292

<212> PRT

<213> Xenopus laevis

<400> 2

Met Ala Ser Asn Arg Gly Gln Leu Asn His Glu Leu Ser Lys Leu Phe
1 5 10 15

Asn Glu Leu Trp Asp Ala Asp Gln Asn Arg Met Lys Ser Gly Lys Asp
20 25 30

Tyr Arg Ile Ser Leu Gln Gly Lys Ala Gly Tyr Val Pro Ala Gly Ser
35 40 45

Asn Gln Ala Arg Asp Ser Ala Ser Phe Pro Leu Phe Gln Phe Val Asp
50 55 60

Glu Glu Lys Leu Lys Ser Arg Lys Thr Phe Ala Thr Phe Ile Ser Leu
65 70 75 80

Leu Asp Asn Tyr Glu Met Asp Thr Gly Val Ala Glu Val Val Thr Pro
85 90 95

Glu Glu Ile Ala Glu Asn Asn Phe Leu Asp Ala Ile Leu Glu Thr
100 105 110

Lys Val Met Lys Met Ala His Asp Tyr Leu Val Arg Lys Asn Gln Ala
115 120 125

Lys Pro Thr Arg Asn Asp Phe Lys Val Gln Leu Tyr Asn Ile Trp Phe
130 135 140

Gln Leu Tyr Ser Arg Ala Pro Gly Ser Arg Pro Asp Ser Cys Gly Phe
145 150 155 160

Arg His Val Phe Val Gly Glu Ser Lys Arg Gly Gln Glu Met Met Gly
165 170 175

Leu His Asn Trp Val Gln Phe Tyr Leu Gln Glu Lys Arg Lys Asn Ile
180 185 190

Asp Tyr Lys Gly Tyr Val Ala Arg Gln Asn Lys Ser Arg Pro Asp Glu
195 200 205

Asp Asp Gln Val Leu Asn Leu Gln Phe Asn Trp Lys Glu Met Val Lys
210 215 220

Pro Val Gly Ser Ser Phe Ile Gly Val Ser Pro Glu Phe Glu Phe Ala
225 230 235 240

Leu Tyr Thr Ile Val Phe Leu Ala Ser Gln Glu Lys Met Ser Arg Glu
245 250 255

Val Val Arg Leu Glu Glu Tyr Glu Leu Gln Ile Val Val Asn Arg His
260 265 270

Gly Arg Tyr Ile Gly Thr Ala Tyr Pro Val Leu Leu Ser Thr Asn Asn
275 280 285

Pro Asp Leu Tyr
290

<210> 3
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic oligoribonucleotide

<220>
<221> misc_RNA
<222> (1)..(20)
<223> Synthetic oligoribonucleotide which includes U16 upstream

cleavage site

<400> 3
ggaaacguau ccuuugggag

20

<210> 4
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<220>
<221> misc_RNA
<222> (1)..(20)
<223> Mutant of SEQ ID 3

<220>
<221> variation
<222> (20)..(20)
<223> "U" is replaced by "T"

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ggaaacguau ccuugggagt

20

<210> 5
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic oligoribonucleotide

<220>
<221> misc_RNA
<222> (1)..(20)
<223> Mutant of SEQ ID 3

<220>
<221> variation
<222> (14)..(14)
<223> "U" is replaced by "C"

<400> 5
ggaaacguau ccucugggag

20

<210> 6
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic oligoribonucleotide

<220>
<221> misc_RNA
<222> (1)..(20)
<223> Mutant of SEQ ID 3

<220>
<221> variation
<222> (14)..(14)
<223> "U" is replaced by "G"

<400> 6
ggaaacguau ccuguggggag 20

<210> 7
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<220>
<221> misc_feature
<222> (1)..(27)
<223> Primer

<400> 7
aagcttcttc atggcggtc ggccaat 27

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> MAHs: synthetic degenerate oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer element

<220>
<221> modified_base
<222> (6)..(6)
<223> "n" : I

<220>
<221> modified_base

<222> (18)..(18)
<223> "n" : I

<400> 8
atggcncayg aytayytngt 20

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> IGTa: synthetic degenerate oligonucleotide

<220>
<221> misc_feature
<222> (1)`..(20)
<223> PCR primer element

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<222> (3)..(3)
<223> "n" : I

<220>
<221> modified_base
<222> (9)..(9)
<223> "n" : I

<220>
<221> modified_base
<222> (12)..(12)
<223> "n": I

<220>
<221> modified_base
<222> (15)..(15)
<223> "n" : I

<220>
<221> modified_base
<222> (18)..(18)
<223> "n" : I

<400> 9
acnggrtang cngtnccnat 20